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9 leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or  
10 45 of JS *cp45*, and/or a mutation in an N gene start sequence at a position corresponding to  
11 nucleotide 62 of JS *cp45*, said genome or antigenome] combined with one or more  
12 heterologous gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of  
13 HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV genome or  
14 antigenome.

1 21. (Twice Amended) The chimeric PIV of claim [6] 1, wherein the  
2 chimeric genome or antigenome incorporates at least one and up to a full complement of  
3 attenuating mutations present within HPIV3 JS *cp45*.

C2  
1 22. (Twice Amended) The chimeric PIV of claim [6] 1, wherein the  
2 chimeric genome or antigenome incorporates at least one and up to a full complement of  
3 attenuating mutations specifying an amino acid substitution in the L protein at a position  
4 corresponding to Tyr<sub>942</sub>, Leu<sub>992</sub>, or Thr<sub>1558</sub> of in JS *cp45*; in the N protein at a position  
5 corresponding to residues Val<sub>96</sub> or Ser<sub>389</sub> of JS *cp45*, in the C protein at a position  
6 corresponding to Ile<sub>96</sub> of JS *cp45*, in the F protein at a position corresponding to residues Ile<sub>420</sub>  
7 or Ala<sub>450</sub> of JS *cp45*, in the HN protein at a position corresponding to residue Val<sub>384</sub> of JS *cp45*,  
8 a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position  
9 corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a mutation in an N gene start  
10 sequence at a position corresponding to nucleotide 62 of JS *cp45*.

C3  
1 39. (Twice Amended) An isolated polynucleotide comprising a chimeric  
2 parainfluenza virus (PIV) genome or antigenome which includes a partial or complete human  
3 parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at least  
4 one and up to a full complement of attenuating mutations present within HPIV3 JS *cp45*  
5 selected from mutations specifying an amino acid substitution in the L protein at a position  
6 corresponding to Tyr<sub>942</sub>, Leu<sub>992</sub>, or Thr<sub>1558</sub> of JS *cp45*; in the N protein at a position  
7 corresponding to residues Val<sub>96</sub> or Ser<sub>389</sub> of JS *cp45*, in the C protein at a position  
8 corresponding to Ile<sub>96</sub> of JS *cp45*, a nucleotide substitution in a 3' leader sequence of the  
9 chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a  
10 mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp45*,

C3 11 said genome or antigenome] combined with one or more heterologous gene(s) or genome  
12 segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of  
13 one or both of HPIV1 and HPIV2 to form a chimeric PIV genome or antigenome.

1 48. (Twice Amended) A method for producing an infectious attenuated  
2 chimeric parainfluenza virus (PIV) particle from one or more isolated polynucleotide  
3 molecules encoding said PIV, comprising:  
4 expressing in a cell or cell-free lysate an expression vector comprising an  
5 isolated polynucleotide comprising a partial or complete human parainfluenza virus 3 JS  
6 (HPIV3 JS) vector genome or antigenome [that incorporates at least one and up to a full  
7 complement of attenuating mutations present within HPIV3 JS *cp45* selected from mutations  
8 specifying an amino acid substitution in the L protein at a position corresponding to Tyr<sub>942</sub>,  
9 Leu<sub>992</sub>, or Thr<sub>1558</sub> of JS *cp45*; in the N protein at a position corresponding to residues Val<sub>96</sub> or  
10 Ser<sub>389</sub> of JS *cp45*, in the C protein at a position corresponding to Ile<sub>96</sub> of JS *cp45*, a nucleotide  
11 substitution in a 3' leader sequence of the chimeric virus at a position corresponding to  
12 nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a mutation in an N gene start sequence at a  
13 position corresponding to nucleotide 62 of JS *cp45*, said genome or antigenome] combined  
14 with one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic  
15 determinant(s) of HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV  
16 genome or antigenome, and PIV N, P, and L proteins.

C5 1 50. (Twice Amended) An expression vector comprising an operably linked  
2 transcriptional promoter, a polynucleotide sequence which includes a partial or complete  
3 human parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at  
4 least one and up to a full complement of attenuating mutations present within HPIV3 JS *cp45*  
5 selected from mutations specifying an amino acid substitution in the L protein at a position  
6 corresponding to Tyr<sub>942</sub>, Leu<sub>992</sub>, or Thr<sub>1558</sub> of JS *cp45*; in the N protein at a position  
7 corresponding to residues Val<sub>96</sub> or Ser<sub>389</sub> of JS *cp45*, in the C protein at a position  
8 corresponding to Ile<sub>96</sub> of JS *cp45*, a nucleotide substitution in a 3' leader sequence of the  
9 chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a  
10 mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp45*,

05 11 said genome or antigenome] combined with one or more heterologous gene(s) or genome  
12 segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of  
13 HPIV1 and/or HPIV2 to form a chimeric PIV genome or antigenome, and a transcriptional  
14 terminator.

Please add new claims 51-52 as follows:

06 1 --51. The chimeric PIV of claim 6, wherein the chimeric genome or  
2 antigenome incorporates at least one and up to a full complement of attenuating mutations  
3 present within HPIV3 JS *cp45* selected from mutations specifying an amino acid substitution  
4 in the L protein at a position corresponding to Tyr942, Leu992, or Thr1558 of JS *cp45*; in the  
5 N protein at a position corresponding to residues Val96 or Ser389 of JS *cp45*, in the C protein  
6 at a position corresponding to Ile96 of JS *cp45*, a nucleotide substitution in a 3' leader sequence  
7 of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*,  
8 and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of  
9 JS *cp45*.

1 52. The isolated polynucleotide of claim 39, wherein the chimeric genome  
2 or antigenome incorporates at least one and up to a full complement of attenuating mutations  
3 present within HPIV3 JS *cp45*--